L Number	Hits	Search Text	DB	Time stamp
1	37280	mass adj spectro$	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 08:48
2	23	2de same gel	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 08:49
3	14	(mass adj spectro$) and (2de same gel)	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 08:58
4	896	two adj dimensional adj gel	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 08:58
5	14	(mass adj spectro$) and (2de same gel)	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 08:59
6	215	(mass adj spectro$) and (two adj dimensional adj gel)	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 08:59
8	9891	hapten	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 08:59
9	11	((mass adj spectro$) same (two adj dimensional adj gel)) and hapten	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 08:59
7	90	(mass adj spectro$) same (two adj dimensional adj gel)	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 09:58
10	399	superdex adj "75"	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 09:58
11	4	((mass adj spectro$) and (two adj dimensional adj gel)) and (superdex adj "75")	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:43
12	2018976	proteome (w) analysis	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:43
13	560	proteomic$	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:43
14	63647	urin$	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:44
15	7435	(proteome (w) analysis) same urin$	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:44
16	56	proteome adj analysis	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:44
17	0	urin$ same (proteome adj analysis)	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:45

18	5	proteomic$ same urin$	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:45
20	0	(two adj dimensional adj gel) and ((mass adj spectro$) and (proteomic$ same urin$))	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:45
21	0	(superdex adj "75") and ((mass adj spectro$) and (proteomic$ same urin$))	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:45
19	3	(mass adj spectro$) and (proteomic$ same urin$)	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:49
22	119	proteomic$ and urin$	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:52
23	92	(mass adj spectro$) and (proteomic$ and urin$)	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:52
24	57623	electrophores$	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:52
25	82	((mass adj spectro$) and (proteomic$ and urin$)) and electrophores$	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:53
26	0	(superdex adj "75") and (((mass adj spectro$) and (proteomic$ and urin$)) and electrophores$)	USPAT; US-PGPUB; EPO; DERWENT	2002/10/15 10:53

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FILE 'CAPLUS, MEDLINE, BIOSIS, CA, SCISEARCH, EMBASE' ENTERED AT 10:00:47
    ON 15 OCT 2002
L1          1806 S PROTEOME (W) ANALYSIS
L2         10581 S PROTEOMIC?
L3        518627 S MASS (W) SPECTROMETRY
L4       1491904 S URIN?
L5             7 S L1 (S) L4
L6             3 DUPLICATE REM L5 (4 DUPLICATES REMOVED)

=> s l3 and l6
L7             2 L3 AND L6

=> d his

     (FILE 'HOME' ENTERED AT 10:00:23 ON 15 OCT 2002)

     FILE 'CAPLUS, MEDLINE, BIOSIS, CA, SCISEARCH, EMBASE' ENTERED AT 10:00:47
     ON 15 OCT 2002
L1          1806 S PROTEOME (W) ANALYSIS
L2         10581 S PROTEOMIC?
L3        518627 S MASS (W) SPECTROMETRY
L4       1491904 S URIN?
L5             7 S L1 (S) L4
L6             3 DUPLICATE REM L5 (4 DUPLICATES REMOVED)
L7             2 S L3 AND L6
```

```
=> s l2 (s) l4
L8          95 L2 (S) L4

=> s l3 and l8
L9          38 L3 AND L8
```

L10 ANSWER 9 OF 14 MEDLINE DUPLICATE 6

TI Peptide mapping of proteins in human body fluids using electrospray ionization Fourier transform ion cyclotron resonance **mass spectrometry**.

AB Human body fluids have been rediscovered in the post-genomic era as great sources of biological markers and perhaps particularly as sources of potential protein biomarkers of disease. Analytical tools that allow rapid screening, low sample consumption, and accurate protein identification are of great importance in studies of complex biological samples and clinical diagnosis. **Mass spectrometry** is today one of the most important analytical tools with applications in a wide variety of fields. One of the fastest growing applications is in **proteomics**, or the study of protein expression in an organism. **Mass spectrometry** has been used to find post-translational modifications and to identify key functions of proteins in the human body. In this study, we review the use of human body fluids as sources for clinical markers and present new data that show the ability of Fourier transform ion cyclotron resonance (FTICR) **mass spectrometry** (MS) to identify and characterize proteins in four human body fluids: plasma, cerebrospinal fluid (CSF), saliva, and **urine**. The body fluids were tryptically digested without any prior separation, purification, or selection, and the digest was introduced into a 9.4 T FTICR mass spectrometer by direct-infusion electrospray ionization (ESI). Even though these samples represent complex biological mixtures, the described method provides information that is comparable with traditional 2D-PAGE data. The sample consumption is extremely low, a few microliters, and the analysis time is only a few minutes. It is, however, evident that the separation of proteins and/or peptides must be included in the methodology, in order to detect low-abundance proteins and other proteins of biological relevance.

SO MASS SPECTROMETRY REVIEWS, (2002 Jan-Feb) 21 (1) 2-15. Ref: 54
Journal code: 8219702. ISSN: 0277-7037.

AU Bergquist Jonas; Palmblad Magnus; Wetterhall Magnus; Hakansson Per;

SWER 11 OF 14 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 8

TI Toward **proteomics** in uroscopy: **Urinary** protein profiles after radiocontrast medium administration

AB Previous attempts to use urinary protein profiles for diagnostic purposes have been rather disappointing with respect to their clin. validity, in part because of the insufficient reproducibility, sensitivity, and rapidity of available techniques. Therefore, a newly developed, high-throughput technique, namely surface-enhanced laser desorption/ionization (SELDI) ProteinChip array-time of flight **mass spectrometry**, was studied, to assess its applicability for protein profiling of urine and to exemplify its use for a group of patients receiving radiocontrast medium. Assessment of the accuracy, sensitivity, and reproducibility of SELDI in test urinary protein profiling was performed. Renal function was studied in 20 male Sprague-Dawley rats before and after i.v. administration of either 1.25 g/kg ioxilan (n = 10) or hypertonic saline soln. (n = 10) as a control. Urine samples from 25 patients undergoing cardiac catheterization were obtained before, immediately after, and 6 to 12 h after the procedure. Administration of ioxilan to rats resulted in changes in the abundance of proteins of 9.9, 18.7, 21.0, and 66.3 kDa. For patients, even in uncomplicated cases of radiocontrast medium infusion during cardiac catheterization, perturbations in the protein compn. occurred but returned to baseline values after 6 to 12 h. Protein with mol. masses of 9.75, 11.75, 23.5, and 66.4 kDa changed in abundance. For patients with impaired renal function, these changes were not reversible within 6 to 12 h. As a proof of principle, one of the peaks, i.e., that at 11.75 kDa, was identified as .beta.2-microglobulin. SELDI is a promising tool for the detection, identification, and characterization of trace amts. of proteins in urine. Even for patients without renal complications, proteins with a broad range of mol. masses either appear in or disappear from the urine. Some of these might represent markers of impending nephropathy.

SO Journal of the American Society of Nephrology (2001), 12(5), 1026-1035
CODEN: JASNEU; ISSN: 1046-6673

AU Hampel, Dierk J.; Sansome, Christine; Sha, Ma; Brodsky, Sergey; Lawson, William E.; Goligorsky, Michael S.

L10 ANSWER 2 OF 14 MEDLINE DUPLICATE 2

TI **Proteomic** analysis of normal human **urinary** proteins isolated by acetone precipitation or ultracentrifugation.

AB BACKGROUND: **Proteomic** techniques have recently become available for large-scale protein analysis. The utility of these techniques in identification of **urinary** proteins is poorly defined. We constructed a proteome map of normal human **urine** as a reference protein database by using two differential fractionated techniques to isolate the proteins. METHODS: Proteins were isolated from **urine** obtained from normal human volunteers by acetone precipitation or ultracentrifugation, separated by two-dimensional polyacrylamide gel electrophoresis (2D-PAGE) and identified by matrix-assisted laser desorption ionization-time-of-flight (MALDI-TOF) **mass spectrometry** followed by peptide mass fingerprinting. RESULTS: A total of 67 protein forms of 47 unique proteins were identified, including transporters, adhesion molecules, complement, chaperones, receptors, enzymes, serpins, cell signaling proteins and matrix proteins. Acetone precipitated more acidic and hydrophilic proteins, whereas ultracentrifugation fractionated more basic, hydrophobic, and membrane proteins. Bioinformatic analysis predicted glycosylation to be the most common explanation for multiple forms of the same protein. CONCLUSIONS: Combining two differential isolation techniques magnified protein identification from human **urine**. **Proteomic** analysis of **urinary** proteins is a promising tool to study renal physiology and pathophysiology and to determine biomarkers of renal disease.

SO KIDNEY INTERNATIONAL, (2002 Oct) 62 (4) 1461-9.
Journal code: 0323470. ISSN: 0085-2538.

AU Thongboonkerd Visith; McLeish Kenneth R; Arthur John M; Klein Jon B